

TABLE S2. BLAST hits obtained from NCBI blastn using 16S rDNA and *gyrB* sequences of representative strains belonging to the different *Enterobacter agglomerans* biotypes defined by Brenner et al. [1].

Biotype	Strain	16S rDNA, best reliable hit(s) ^a	Accession	% Match	<i>gyrB</i> , best reliable hit(s) ^a	Accession	% Match
I	LMG 1286	<i>Pantoea agglomerans</i> NCTC9381T	AJ251466.1	1505/1515 (99%)	<i>Pantoea agglomerans</i> LMG 2554	EF988811.1	733/741 (98%)
II	LMG 5345	<i>Erwinia tasmaniensis</i> ET1/99	CU468135.1	1438/1471 (97%)	<i>Pantoea</i> sp. LMG 24200 <i>Enterobacter sakazakii</i> BAA-894 <i>Erwinia tasmaniensis</i> ET1/99	EF988770.1 CP000783.1 NC_010694	664/745 (89%) 654/746 (87%) 629/740 (85%)
III	LMG 2605	<i>Pantoea dispersa</i> GTC 1472	AB273743.1	1460/1465 (99%)	<i>Pantoea dispersa</i> LMG 2603	EF988818.1	730/740 (98%)
IV	ATCC 27998	<i>Erwinia soli</i> Ew02 <i>Erwinia tasmaniensis</i> strain ET1/99	EF540891.1 CU468135.1	1404/1423 (98%) 1425/1470 (96%)	<i>Salmonella enterica</i> subsp. <i>enterica</i> sv. Schwarzengrund CVM19633	CP001127.1	628/724 (86%)
V	LMG 5343	<i>Pantoea agglomerans</i> LMG 2565	AF373196	1448/1476 (98%)	<i>Pantoea agglomerans</i> LMG 2565	EF988814.1	674/744 (90%)
VI	LMG 5342	<i>Pantoea ananatis</i> LMG 2665	Z96081	1343/1362 (98%)	<i>Pantoea ananatis</i> LMG 2665	EF988824.1	738/740 (99%)
VII	LMG 5336	<i>Enterobacter</i> sp. 638	CP000653	1442/1464 (98%)	<i>Enterobacter cloacae</i> ATCC 13047 <i>Citrobacter koseri</i> ATCC BAA-895	AB084011.1 CP000822.1	674/724 (93%) 661/722 (91%)
VIII	LMG 5341	<i>Erwinia persicinus</i>	AJ001190.1	1457/1464 (99%)	<i>Erwinia pyrifoliae</i> DSM12163	AB242885.1	672/740 (90%)
IX	ATCC 29918	<i>Escherichia hermannii</i> GTC 347 <i>Salmonella typhimurium</i> LT2	AB273738.1 AE008706.1	1451/1468 (98%) 1443/1467 (98%)	<i>Salmonella enterica</i> subsp. <i>enterica</i> sv. Heidelberg SL476	CP001120.1	668/737 (90%)
X	LMG 5339	<i>Buttiauxella agrestis</i> DSM 4586	AJ233400.1	1442/1449 (99%)	<i>Enterobacter sakazakii</i> ATCC BAA-894	CP000783.1	689/815 (84%)
XI	LMG 5338 ^b	-	-	-	-	-	-
XII	LMG 5337	<i>Klebsiella pneumoniae</i> MGH 78578 <i>Citrobacter koseri</i> ATCC BAA-895 <i>Salmonella enterica</i> subsp. <i>enterica</i> sv. Heidelberg SL476	CP000647.1 CP000822 CP001120	1424/1466 (97%) 1421/1465 (96%) 1420/1466 (96%)	<i>Citrobacter koseri</i> ATCC BAA-895 <i>Salmonella enterica</i> subsp. <i>arizonae</i>	CP000822.1 CP000880.1	674/743 (90%) 663/729 (90%)
XIII	EL107 ^c	<i>Pantoea agglomerans</i> LMG 2565	AF373196.1	1466/1477 (99%)			

^a Self-hits are excluded, only hits to established strains with accepted species name were considered. Hits complete sequenced organisms were preferred.

^b No sequence available, but according to Tamura et al. [2] strains of biotype XI belongs to *Leclercia adecarboxylata*.

^c 16S rDNA sequence of *P. agglomerans* EL107 was retrieved in the NCBI database under accession number FJ357815.

References

1. Brenner DJ, Fanning GR, Leete Knutson JK, Steigerwalt AG, Krichevsky MI: **Attempts to classify Herbicola group-*Enterobacter agglomerans* strains by deoxyribonucleic acid hybridization and phenotypic tests.** *Int J Syst Bacteriol* 1984, **34**(1):45-55.
2. Tamura K, Sakazaki R, Kosako Y, Yoshizaki E: ***Leclercia adecarboxylata* gen. nov., comb. nov., formerly known as *Escherichia adecarboxylata*.** *Curr Microbiol* 1986, **13**:179-184.